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gccgtct	t	gg	c	ct	g	aggg	g	g	g	g	g	g	g	g	1140
gcctac	c	t	c	c	t	c	c	c	c	c	c	c	c	c	1200
gagtg	g	a	c	g	c	c	c	c	c	c	c	c	c	c	1260
cttaag	c	g	a	a	c	g	a	a	c	g	a	a	c	g	1320
ctctccc	g	g	g	g	g	g	g	g	g	g	g	g	g	g	1380
caggcc	c	t	t	t	c	c	c	t	t	c	c	c	c	c	1440
ttggc	g	g	g	g	g	g	g	g	g	g	g	g	g	g	1500
gagct	t	a	g	g	c	c	c	c	c	c	c	c	c	c	1560
gcggt	g	c	t	g	c	t	g	g	a	a	a	a	a	a	1620
gagct	c	a	c	c	a	a	a	a	a	a	a	a	a	a	1680
acggg	c	c	c	c	c	c	c	c	c	c	c	c	c	c	1740
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gccttc	g	t	g	g	g	g	g	g	g	g	g	g	g	g	1860
cg	g	c	t	c	c	t	c	c	c	c	c	c	c	c	1920
gacat	c	c	c	a	c	c	a	c	c	c	c	c	c	c	1980
ctgat	g	c	g	c	c	c	c	c	c	c	c	c	c	c	2040
aggct	c	t	c	c	c	c	c	c	c	c	c	c	c	c	2100
ttccaa	a	g	c	t	c	c	c	c	c	c	c	c	c	c	2160
cg	g	g	g	g	g	g	g	g	g	g	g	g	g	g	2220
gtga	a	g	a	g	a	g	a	g	a	g	a	g	a	g	2280
gccgc	c	c	g	a	c	c	c	c	c	c	c	c	c	c	2340
gccc	g	c	a	t	g	c	c	c	c	c	c	c	c	c	2400
gagg	a	g	g	t	g	g	c	t	t	t	g	g	c	c	2460
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<210> 408

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 408

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			20					25						30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	
			35				40					45				
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	
	50					55					60					
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	
65					70					75					80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	
				85					90					95		
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	
			100					105					110			
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	
			115				120					125				
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	
	130					135					140					
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	
145					150				155						160	
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	
				165					170					175		
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	
			180					185					190			
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	
		195					200					205				
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	
	210					215					220					
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	
225					230					235					240	
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	
				245					250					255		
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	
			260					265					270			
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	
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Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
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Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
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Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
325 330 335
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
340 345 350
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
355 360 365
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
370 375 380
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
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Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
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His Arg Asn Leu Leu Lys Arg Asn Glu Gly Lys Glu Lys Leu Leu Trp
420 425 430
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Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
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Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
515 520 525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
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Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545 550 555 560
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
565 570 575
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
580 585 590
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
595 600 605
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
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 820 825 830
 Ser Ala Lys Gly
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<210> 409

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 409

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tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc	300
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<210> 410

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 410

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Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
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 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
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 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
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 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
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 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
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 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Phe Glu Gly Glu Glu Lys Leu Leu Cys
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 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
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 465 470 475 480
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 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
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Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
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 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
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 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
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 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
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 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
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 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
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 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
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 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
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 820 825 830
 Ser Ala Lys Gly
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<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

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<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 412

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			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				

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 Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
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 Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
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 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
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 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Phe Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
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 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 413

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> n

<222> (19) .. (21)

<223> n is any base a,t,c, or g.

<400> 413

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42

<210> 414

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 414

cctaagctcg tcaaagag

18

<210> 415

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 415

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac    180
gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttcgg ccacgaggcc    240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc    300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag    360
gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgagggtcgc    420
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cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag    540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cgggggtcaag    600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc    660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg    720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg    780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg    840
gagttcgcca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag    900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc    960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca   1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc   1080
gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgaccc catgctctc   1140
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caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttcgc   1440
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 gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
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 ctgatgcgcc gggcgggcaa gacggtgaac ttcggcgctc tctacggcat gtccgcccac 2040
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 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
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 gaggaggtgg cggttttggc caaggaggcc atggagaagg cctatccctc cgccgtgccc 2460
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<210> 416

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 416

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75				80	

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95
 Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Val Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830

Ser Ala Lys Gly
 835

<210> 417

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 417

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaagccc cctccttcgc ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccc acccccaggg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctcg accgcgtcgc cgtcctccac	480
cccaggggcc acctcatcac ccgggagtgg ctttgggaga agtacggcct caggccggag	540
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ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcgga gcctcctcca cgagttcggc ctctggagg cccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tctctcccc ccccgagccc	960

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gccgtctt	ggcctgagg	ggggctag	acctgtgcc	gggacgac	catgctc	ctc	1140
gcctacct	cttgaccct	gaacacc	accgaggg	tgccgcgg	ctacgggg		1200
gagtggac	ggagcgcc	ccaccggg	ctcctctc	agaggctc	tcggaac	ctc	1260
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gagcttag	gtccagttt	gaagaag	acagacag	gcaagcg	caccagc	gcc	1560
gcgggtgt	ggccctac	ggaggccc	cccatcgt	agaagat	ccagcac	cg	1620
gagctcac	agctcaag	cacctac	gtgaccc	ctcgt	ccaccgc	agg	1680
acgggccc	gtcacacc	cttcaacc	agggccac	ccacgggg	gcttagt	agc	1740
tcggaccca	acctgcag	catcccc	gtccccc	tgggccag	gatccgc	cg	1800
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ctgatgc	ggggggcca	gacgggt	gaacttc	gttcgggt	gtccgcc	cat	2040
aggctct	cccaggct	gtacccct	acgaggcg	tgcccttt	atagagc	tac	2100
ttccaaag	ctcccaag	gcgggcct	gtatagaa	ccctggag	ggggagg	aag	2160
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gtgaagag	ctagggag	cgccgag	cgcatgt	acatgcc	ccagggc	acc	2280
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gcccgc	atctccag	cgccaac	gagctc	agggcccc	agcgggg	gcc	2400
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<210> 418

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 418

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
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Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
245 250 255
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
260 265 270
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
290 295 300
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305 310 315 320
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
325 330 335
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
340 345 350
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
355 360 365
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
370 375 380
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385 390 395 400
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
405 410 415
His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
420 425 430
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
435 440 445
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
450 455 460
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465 470 475 480
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
485 490 495
Val Leu Phe Asp Glu Leu Arg Leu Pro Ser Leu Lys Lys Thr Lys Lys
500 505 510
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
515 520 525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
530 535 540
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545 550 555 560
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
565 570 575
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
580 585 590
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
595 600 605
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 419

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 419

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaagccc cctccttcgc ccacgaggcc	240

tacgaggcct acaaggcggg gagggccccc acccccgagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgagggtgcgc	420
atcctcaccg ccgaccgga cctctaccaa ctctgtctccg accgcgtcgc cgtcctccac	480
cccagaggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag	600
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<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 420

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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
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 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
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 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
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 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
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 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
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 450 455 460
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 465 470 475 480
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Thr Gly Lys Arg Ser Thr Gly Ala Ala Val Leu Glu Ala Leu Arg Glu
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 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
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 740 745 750
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 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
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 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
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<210> 424

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 424

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
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 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
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 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
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 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
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 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
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 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Leu Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
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 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
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 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
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 Ser Ala Lys Gly
 835

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			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75					80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
			100					105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145					150				155						160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
225					230					235					240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
				245					250					255	

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Arg Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

<400> 428

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ccggtgcagg	cgggtctacg	cttcgccaag	agcctcctca	aggccctcaa	ggaggacggg	180
gacgcggtga	tcgtggtctt	tgacgccaag	gccccctcct	tccgccacga	ggcctacggg	240
gggtacaagg	cgggcccggc	ccccacggcg	gaggactttc	cccggcaact	cgccctcatc	300
aaggagctgg	tggacctcct	ggggctggcg	cgctctgagg	tcccgggcta	cgaggcggac	360
gacgtcctgg	ccagcctggc	caagaaggcg	gaaaaggagg	gctacgaggt	ccgcctcctc	420
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gggtacctca	tcaccccggc	ctggcttttg	gaaaagtagc	gcctgaggcc	cgaccagtgg	540
gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccggggg	caagggcatc	600
ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccacat	ggacgatctg	720
aagctctcct	gggacctggc	caaggtgcgc	accgacctgc	ccctggaggt	ggacttcgcc	780
aaaaggcggg	agcccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttggc	840
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gccctgaggg	aaggccttgg	cctcccgcgc	ggcgacgacc	ccatgctcct	cgcctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcccggc	gctacggcgg	ggagtggacg	1200
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cttgaggggg	aggagaggct	ccttttgctt	taccgggagg	tggagaggcc	cctttccgct	1320
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cacccttcca	acctcaactc	ccgggaccag	ctggaaaggg	tcctctttga	cgagctaggg	1500
cttcccgcga	tcaagaagac	gcaaaagacc	ggcaagcgct	ccaccagcgc	cgccgtcctg	1560
gaggccctcc	gcgaggccca	ccccatcggt	gagaagatcc	tgcagtaccg	ggagctcacc	1620
aagctgaaga	gcacctacat	tgacctcttg	ccggacctca	tccaccccag	gacgggcccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggca	ggctaagtag	ctccgatccc	1740
aacctccaga	acatccccgt	ccgcaccccg	cttgggcaga	ggatccgccc	ggccttcac	1800
gccgaggagg	ggtggctatt	ggtggccctg	gactatagcc	agatagagct	caggggtgctg	1860

gccacacct cccgacga gaacctgac cgggtcttcc aggagggcg ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980
 cgggcggcca agaccatcaa cttcgggggtc ctctacggca tgcggccca cgcctctcc 2040
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 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
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 gtgcgggagg cggccgagcg catggccttc aacatgccc tccagggcac cgccgccgac 2280
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 ctcttcagg tcgccaacga gctggctctc gagggcccaa aagagagggc ggaggccgtg 2400
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<210> 429

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 429

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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35				40						45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65				70					75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85					90						95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Gln Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu

<210> 430

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 430

acgggggtgc gccgggacgt ggcctat

27

<210> 431

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 431

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gaaccgggtgc aggcgggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg cegtcttcgt ggtctttgac gccaaaggccc cctccttcgg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccc acccccaggg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgga cctctaccaa ctcgctcccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac ccgggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggaggtg	780

gacctcgccc aggggcgggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
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cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag	1920
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ttccaaagct tccccaaagt gcgggcctgg atagaaaaga ccctggagga ggggaggaag	2160
cggggctacg tggaaaccct ctccggaaga aggcgctacg tgcccaccc caacgcccgg	2220
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gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccc cgccgtgccc	2460
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<210> 432

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 432

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
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20 25 30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Lys Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 433

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 433		
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<210> 434		
<211> 36		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic		
<400> 434		
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<210> 435		
<211> 2508		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic		
<400> 435		
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ggccaccacc tggcctaccg cacttcttcc gccctgaagg gcctcaccac gagccggggc	120	
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180	
gggtacaagg ccgtcttcgt ggtctttgac gccaaagccc cctccttcgc ccacgaggcc	240	
tacgaggcct acaaggcggg gagggccccg acccccgagg acttccccgc gcagctcgcc	300	
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggctcc cggctacgag	360	
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420	
atcctcaccg ccgaccgga cctctaccaa ctctgtctcc accgcgtcgc cgtcctccac	480	
cccgagggcc acctcatcac ccgggagtgg ctttgggaga agtacggcct caggccggag	540	
cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag	600	
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ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggccacctg	720	
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780	
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840	
gagttcggca gcctcctcca cgagttcggc ctctggagg ccccgcccc cctggaggag	900	
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc	960	

atgtgggagg	agcttaaagc	cctggccgcc	tgcaggggag	gccgcgtgca	ccgggcagca	1020
gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
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gcccgcacgc	tcctccaggt	cgccaacgag	ctcctccttg	aggcccccca	agcgcggggc	2400
gaggaggtgg	cggttttggc	caaggaggcc	atggagaagg	cctatccccct	cgccgtgccc	2460
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<210>	436					
<211>	836					
<212>	PRT					

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 436

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
245 250 255
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
260 265 270
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
290 295 300
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305 310 315 320
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
325 330 335
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
340 345 350
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
355 360 365
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
370 375 380
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385 390 395 400
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
405 410 415
His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
420 425 430
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
435 440 445
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
450 455 460
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465 470 475 480
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
485 490 495
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
500 505 510
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
515 520 525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
530 535 540
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545 550 555 560
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
565 570 575
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
580 585 590
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
595 600 605
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile Ala Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 437

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 437

gaggggaagg acatcgccac ccagaccgca agc

33

<210> 438

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 438

gcttgcggtc tgggtggcga tgccttccc etc

33

<210> 439

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 439

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgctctcgt ggtctttgac gccaaggccc cctccttcgg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccaggg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccggcc tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgga cctctaccaa ctctctccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cgggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttccct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctctggagg cccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tctctcccc ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcagggggc gccgcgtgca ccgggcagca	1020

gaccccttgg	cggggctaaa	ggacctcaag	gagggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgagggg	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccagggggg	tggcgcgggc	ctacgggggg	1200
gagtggacgg	aggacgcgc	ccaccggggc	ctcctctcgg	agaggctcca	tcggaacctc	1260
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cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgtcc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgtcc	tctacggcat	gtccgcccac	2040
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cggggctacg	tggaaaccct	cttcggaaga	aggcgctacg	tgccccacct	caacgcccgg	2220
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gccgccgacc	tcatgaagct	cgccatggtg	aagctcttcc	cccgcctccg	ggagatgggg	2340
gcccgcacgc	tctccaggt	cgccaacgag	ctcctcctgg	aggcccccca	agcgcggggc	2400
gaggaggtgg	cggctttggc	caaggaggcc	atggagaagg	cctatcccct	cgcctgccc	2460
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<210> 440

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 440

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	210	215	220	
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	225	230	235	240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	245	250	255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	260	265	270	
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	275	280	285	
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	290	295	300	
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	305	310	315	320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
325 330 335
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
340 345 350
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
355 360 365
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
370 375 380
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385 390 395 400
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
405 410 415
His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
420 425 430
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
435 440 445
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
450 455 460
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465 470 475 480
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
485 490 495
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Pro Lys Lys
500 505 510
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
515 520 525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
530 535 540
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545 550 555 560
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
565 570 575
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
580 585 590
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
595 600 605
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
610 615 620
His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625 630 635 640
Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
645 650 655

<400> 442
 cttgcctgtc ttcttcggct tcttcaaggc ggg

33

<210> 443

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 443

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ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggcccggc cccacgcgc gaggactttc cccggcaact cgcctcatc	300
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aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc	840
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 cttttgcagg tgcacaacga actggtcctc gaggtccca aggagcaagc ggaggaagtc 2400
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 gaagtgggca tcggggagga ctggctttcc gccaaaggcc 2499

<210> 444

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 444

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val Tyr Arg Ala
 325 330 335
 Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu
 355 360 365
 Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn	Thr	Ala	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	385	390	395	400
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Tyr	Ala	Ala	405	410	415	
Leu	Leu	Lys	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu	420	425	430	
Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	435	440	445	
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Lys	Ala	Leu	Ser	Leu	Glu	Val	450	455	460	
Glu	Ala	Glu	Ile	Arg	Arg	Phe	Glu	Glu	Glu	Val	His	Arg	Leu	Ala	Gly	465	470	475	480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Ile	Phe	485	490	495	
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Lys	Lys	Thr	Arg	Lys	Thr	Gly	Lys	500	505	510	
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	515	520	525	
Ile	Val	Asp	Arg	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Ser	Lys	Leu	Lys	Gly	530	535	540	
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Ala	Leu	Val	His	Pro	Lys	Thr	Asn	Arg	545	550	555	560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590	
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Arg	Leu	Val	595	600	605	
Val	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	610	615	620	
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Gln	Asp	Ile	His	625	630	635	640
Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	645	650	655	
Ser	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	660	665	670	
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gly	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	675	680	685	
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Tyr	Pro	Lys	Val	690	695	700	
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Ala	Glu	Gly	Arg	Glu	Arg	Gly	Tyr	705	710	715	720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser
725 730 735
Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765
Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val
770 775 780
His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val
785 790 795 800
Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val
805 810 815
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Ala

<210> 445

<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 445

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ccggtgcagg cgggtctacgg ctccgccaaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggccctacggg 240
gggtacaagg cgggcccgggc cccacgcgcg gaggactttc cccggcaact cgcctcatc 300
aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
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gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
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aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780

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gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcaac aagccccggtt	1020
gaggccctgg ccgacctcaa ggaggcccg gggttcctgg ccaaggacct ggccgttttg	1080
gccctgcggg aggggggtgg cctggacccc acggacgacc ccctcctggt ggccctacctc	1140
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ccggtgaagc ggacgaagaa gacgggcaag cgctccaccg cccagggggc cctggaggcc	1560
ctccgggggg cccaccccat cgtggagctc atcctccagt accgggagct ttccaagctc	1620
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caagtggcca acgagctggt cctggagggtg cccgaggacc gggccgagga ggccaaggcc	2400
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<210> 446

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 446

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20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305 310 315 320
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
325 330 335
Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala Arg Gly Phe
340 345 350
Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Val Ala Leu
355 360 365
Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu Asp Pro Ala
370 375 380
Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Phe Thr
385 390 395 400
Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Gln Asn
405 410 415
Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr Gln Glu Val
420 425 430
Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Arg Gly Val
435 440 445
Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu Leu Glu Lys
450 455 460
Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala Gly His Pro
465 470 475 480
Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
485 490 495
Leu Gly Leu Thr Pro Val Lys Arg Thr Lys Lys Thr Gly Lys Arg Ser
500 505 510
Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His Pro Ile Val
515 520 525
Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Ser Thr Tyr
530 535 540
Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly Arg Leu His
545 550 555 560
Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
565 570 575
Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
580 585 590

Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu Leu Ala Ala
 595 600 605
 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
 610 615 620
 Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile His Thr Glu
 625 630 635 640
 Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val Asp Pro Lys
 645 650 655
 Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met
 660 665 670
 Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr Lys Glu Ala
 675 680 685
 Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala
 690 695 700
 Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly Tyr Val Glu
 705 710 715 720
 Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg Val
 725 730 735
 Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
 740 745 750
 Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val Lys Leu Phe
 755 760 765
 Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln Val Ala Asn
 770 775 780
 Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu Ala Lys Ala
 785 790 795 800
 Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp Val Pro Leu
 805 810 815
 Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala Lys Gln Asp
 820 825 830

<210> 447

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 447
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atcctcaccg ccgaccgga cctctaccaa ctctctccg accgcgtcgc cgtcctccac 480
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 ctgatgcgcc gggcggccaa gaccatcaac ttcggcgtcc tctacggcat gtccgcccac 2040
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<210> 448

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 448

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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75				80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
			85						90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
		100						105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 Tyr Arg Ala Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly
 355 360 365
 Ile Ala Leu Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 Tyr Ala Ala Leu Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp
 420 425 430
 Leu Tyr Glu Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser
 450 455 460

Leu Glu Val Glu Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Ile Phe Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys
 530 535 540
 Leu Lys Gly Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys
 545 550 555 560
 Thr Asn Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp
 595 600 605
 Arg Leu Val Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Ala Ser Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala
 785 790 795 800

Glu Glu Val Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro
805 810 815
Leu Lys Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu
820 825 830
Ser Ala Lys Ala
835

<210> 449

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 449

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Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
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Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
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 Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly
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 645 650 655

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 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr
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 690 695 700
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<212> DNA

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cggggctacg tggaaacctt cttcggaaga aggcgctacg tgcccacact caacgcccgg	2220
gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc	2280
gccgcgcacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg	2340
gcccgcacgc tcctccaggt cgccaacgag ctctctctgg agggccccca agcgcggggc	2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatccccct cgccgtgccc	2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac	2520
caccac	2526

<210> 456

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 456

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Lys	Pro	Ser	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	195	200	205	
Lys	Leu	Ile	Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	210	215	220	
Glu	Gln	Val	Lys	Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	225	230	235	240
Glu	Asp	Leu	Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu	245	250	255	
Leu	Leu	Gln	Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	260	265	270	
Leu	Lys	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	275	280	285	
Phe	Gly	Leu	Leu	Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	290	295	300	
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	305	310	315	320

Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Trp Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His
 835 840

<210> 457

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 457

ttccaggtgc ttgaggaggt tttccag

27

<210> 458

<211> 27

<212> DNA

<213> Artificial Sequence .

<220>

<223> Synthetic

<400> 458
ctcctcaagc acctggaaca ggtgaaa

27

<210> 459

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 459
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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttccg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg tttaccgccg tcgagggtccc cggctacgag 360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtgcg 420
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cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cgggggtcaag 600
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 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
 caccac 2526

<210> 460

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 460

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60
Val Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu
210 215 220
Glu Gln Val Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met
225 230 235 240
Glu Asp Leu Lys Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu
245 250 255
Leu Leu Gln Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly
260 265 270
Leu Lys Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
275 280 285
Phe Gly Leu Leu Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro
290 295 300
Pro Pro Glu Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro
305 310 315 320
Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val
325 330 335
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
340 345 350
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
355 360 365
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
370 375 380

Asp 385	Pro	Ser	Asn	Thr	Thr 390	Pro	Glu	Gly	Val	Ala 395	Arg	Arg	Tyr	Gly	Gly 400
Glu	Trp	Thr	Glu	Asp 405	Ala	Ala	His	Arg	Ala 410	Leu	Leu	Ser	Glu	Arg	Leu 415
His	Arg	Asn 420	Leu	Leu	Lys	Arg	Leu	Glu 425	Gly	Glu	Glu	Lys	Leu 430	Leu	Trp
Leu	Tyr	His 435	Glu	Val	Glu	Lys	Pro 440	Leu	Ser	Arg	Val	Leu 445	Ala	His	Met
Glu	Ala 450	Thr	Gly	Val	Arg	Arg 455	Asp	Val	Ala	Tyr	Leu 460	Gln	Ala	Leu	Ser
Leu 465	Glu	Leu	Ala	Glu	Glu 470	Ile	Arg	Arg	Leu	Glu 475	Glu	Glu	Val	Phe	Arg 480
Leu	Ala	Gly	His 485	Pro	Phe	Asn	Leu	Asn 490	Ser	Arg	Asp	Gln	Leu 495	Glu	Arg
Val	Leu	Phe	Asp 500	Glu	Leu	Arg	Leu	Pro 505	Ala	Leu	Lys	Lys	Thr 510	Lys	Lys
Thr	Gly	Lys 515	Arg	Ser	Thr	Ser	Ala 520	Ala	Val	Leu	Glu	Ala 525	Leu	Arg	Glu
Ala	His 530	Pro	Ile	Val	Glu	Lys 535	Ile	Leu	Gln	His	Arg 540	Glu	Leu	Thr	Lys
Leu 545	Lys	Asn	Thr	Tyr	Val 550	Asp	Pro	Leu	Pro	Ser 555	Leu	Val	His	Pro	Arg 560
Thr	Gly	Arg	Leu	His 565	Thr	Arg	Phe	Asn	Gln 570	Thr	Ala	Thr	Ala	Thr	Gly 575
Arg	Leu	Ser	Ser 580	Ser	Asp	Pro	Asn	Leu 585	Gln	Asn	Ile	Pro 590	Val	Arg	Thr
Pro	Leu	Gly 595	Gln	Arg	Ile	Arg	Arg	Ala 600	Phe	Val	Ala	Glu 605	Ala	Gly	Trp
Ala 610	Leu	Val	Ala	Leu	Asp 615	Tyr	Ser	Gln	Ile	Glu 620	Leu	Arg	Val	Leu	Ala
His 625	Leu	Ser	Gly	Asp	Glu 630	Asn	Leu	Ile	Arg	Val 635	Phe	Gln	Glu	Gly	Lys 640
Asp	Ile	His	Thr 645	Gln	Thr	Ala	Ser	Trp	Met 650	Phe	Gly	Val	Pro 655	Pro	Glu
Ala	Val	Asp 660	Pro	Leu	Met	Arg	Arg	Ala 665	Ala	Lys	Thr	Val	Asn 670	Phe	Gly
Val	Leu	Tyr 675	Gly	Met	Ser	Ala	His 680	Arg	Leu	Ser	Gln	Glu 685	Leu	Ala	Ile
Pro	Tyr 690	Glu	Glu	Ala	Val	Ala	Phe 695	Ile	Glu	Arg	Tyr 700	Phe	Gln	Ser	Phe
Pro 705	Lys	Val	Arg	Ala	Trp 710	Ile	Glu	Lys	Thr	Leu 715	Glu	Glu	Gly	Arg	Lys 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His
 835 840

<210> 461

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 461

gtccaggttc ttgaggaggt tttccag

27

<210> 462

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 462

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27

<210> 463

<211> 2532

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 463

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttcg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccagg acttccccg gcagctcgcc	300
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ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
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 cgggccgagg aggtggcgcc tttggccaag gaggccatgg agaaggccta tcccctcgcc 2460
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 caccaccacc ac 2532

<210> 464

<211> 844

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 464

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
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 20 25 30
 Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45
 Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60
 Val Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80
 Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu
 225 230 235 240
 Glu Asp Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu
 260 265 270
 Glu Gly Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu
 275 280 285
 His Glu Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro
 290 295 300
 Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys
 305 310 315 320
 Glu Pro Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly
 325 330 335
 Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys
 340 345 350
 Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg
 355 360 365
 Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr
 370 375 380
 Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr
 385 390 395 400
 Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu
 405 410 415
 Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu
 420 425 430

Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala
 435 440 445
 His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala
 450 455 460
 Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val
 465 470 475 480
 Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu
 485 490 495
 Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr
 500 505 510
 Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu
 515 520 525
 Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu
 530 535 540
 Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His
 545 550 555 560
 Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala
 565 570 575
 Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val
 580 585 590
 Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala
 595 600 605
 Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val
 610 615 620
 Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu
 625 630 635 640
 Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro
 645 650 655
 Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn
 660 665 670
 Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu
 675 680 685
 Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln
 690 695 700
 Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly
 705 710 715 720
 Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val
 725 730 735
 Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg
 740 745 750
 Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys
 755 760 765

Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg
770 775 780

Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala
785 790 795 800

Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala
805 810 815

Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp
820 825 830

Trp Leu Ser Ala Lys Gly His His His His His His
835 840

<210> 465

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 465
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27

<210> 466

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 466
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27

<210> 467

<211> 2532

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 467

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttcg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg ttaccgccg tcgagggtccc cggtacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtgcgc	420
atcctcaccg ccgaccgga cctctacca ctcgtctccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccgaaggac gtccaggaga agtacggggt gccccggag	540
cgctgggtgg acttcgcgc cctcacgggg gaccgctcgg acaacatccc cggggtggcg	600
gggatagggg agaagaccgc cttcgactc ctgcagagt gggggagcgt ggaaaacctc	660
ctgaagaacc tggaccgggt aaagccggac tcgctccggc gcaagataga ggcgcacctc	720
gaggacctcc acctctcctt agacctggcc cgcctccgca ccgacctccc cctggaggtg	780
gactttaagg ccttgcgcg caggaccccc gacctggagg gcctgagggc ctttttggag	840
gagctggagt tcggaagcct cctccacgag ttccggcctcc tgggagggga gaagccccgg	900
gaggaggccc cctggcccc gcccgaggg gccttcgtgg gcttcctcct tccccgaag	960
gagcccatgt gggcgagct tctggccctg gcggcgccct cgggcggccg cgtgcaccgg	1020
gcagcagacc ccttggcggg gctaaaggac ctcaaggagg tccggggcct cctcgccaag	1080
gacctcgccg tcttggcctc gagggagggg ctagacctcg tgcccgggga cgaccccatg	1140
ctcctcgctt acctcctgga ccttcgaac accacccccg agggggtggc gcggcgctac	1200
gggggggagt ggacggagga cgccgccac cgggccctcc tctcgagag gctccatcgg	1260
aacctcctta agcgcctcga ggggaggag aagctccttt ggctctacca cgagggtgaa	1320
aagccctct cccgggtcct ggcccatatg gaggccaccg gggtagggcg ggacgtggcc	1380
taccttcagg ccttttcctt ggagcttgcg gaggagatcc gccgcctcga ggaggaggtc	1440
ttccgcttgg cgggccaccc cttcaacctc aactcccggg accagctgga aagggtgctc	1500
tttgacgagc ttaggcttcc cgccttgaag aagacgaaga agacaggcaa gcgtccacc	1560
agcgccgcgg tgctggaggc cctacgggag gccacccca tcgtggagaa gatcctccag	1620
caccgggagc tcaccaagct caagaacacc tacgtggacc cctcccaag cctcgtccac	1680
ccgaggacgg gccgcctcca caccgcttc aaccagacgg ccacggccac ggggaggctt	1740
agtagctccg accccaacct gcagaacatc cccgtccgca ccccttggg ccagaggatc	1800
cgccgggcct tcgtggccga ggcgggttgg gcgttggtgg ccttgacta tagccagata	1860

gagctccgcg tcctcgccca cctctccggg gacgaaaacc tgatcagggt cttccaggag 1920
 gggaaggaca tccacaccca gaccgcaagc tggatgttcg gcgtccccc ggaggccgtg 1980
 gaccccccta tgcgccgggc ggccaagacg gtgaacttcg gcgtcctcta cggcatgtcc 2040
 gcccataggc tctcccagga gcttgccatc ccctacgagg aggcggtggc ctttatagag 2100
 cgctacttcc aaagcttccc caaggtgcgg gcctggatag aaaagaccct ggaggagggg 2160
 aggaagcggg gctacgtgga aaccctcttc ggaagaaggc gctacgtgcc cgacctcaac 2220
 gcccggtgga agagcgtcag ggaggccgcg gagcgcatgg ccttcaacat gcccgccag 2280
 ggcaccgccg ccgacctcat gaagctcgcc atggtgaagc tcttcccccg cctccgggag 2340
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 cgggcccagg aggtggcggc tttggccaag gaggccatgg agaaggccta tcccctcgcc 2460
 gtgcccctgg aggtggagggt ggggatgggg gaggactggc tttccgcaa gggtcaccac 2520
 caccaccacc ac 2532

<210> 468

<211> 844

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 468

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75				80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
			85						90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
		100					105						110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly
 165 170 175
 Val Pro Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg
 180 185 190
 Ser Asp Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Arg Leu Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu
 225 230 235 240
 Glu Asp Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu
 260 265 270
 Glu Gly Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu
 275 280 285
 His Glu Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro
 290 295 300
 Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys
 305 310 315 320
 Glu Pro Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly
 325 330 335
 Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys
 340 345 350
 Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg
 355 360 365
 Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr
 370 375 380
 Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr
 385 390 395 400
 Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu
 405 410 415
 Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu
 420 425 430
 Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala
 435 440 445
 His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala
 450 455 460

Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val
 465 470 475 480
 Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu
 485 490 495
 Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr
 500 505 510
 Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu
 515 520 525
 Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu
 530 535 540
 Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His
 545 550 555 560
 Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala
 565 570 575
 Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val
 580 585 590
 Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala
 595 600 605
 Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val
 610 615 620
 Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu
 625 630 635 640
 Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro
 645 650 655
 Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn
 660 665 670
 Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu
 675 680 685
 Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln
 690 695 700
 Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly
 705 710 715 720
 Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val
 725 730 735
 Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg
 740 745 750
 Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys
 755 760 765
 Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg
 770 775 780
 Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala
 785 790 795 800

Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala
805 810 815
Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp
820 825 830
Trp Leu Ser Ala Lys Gly His His His His His His
835 840

<210> 469

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 469

ctcgaggcgg gtaaacccca ggaggtc

27

<210> 470

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 470

gggtttaccg gcctcgaggt gcccggc

27

<210> 471

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 471

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60

ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc

120

gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac

180

gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttcg ccacgaggcc

240

tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc

300

ctcatcaagg agctggtgga cctcctgggg tttacccgcc tcgaggtgcc gggctttgaa	360
gcggatgacg tcctggctac cctggccaag aaggcggaaa aggaaggcta cgaagtgcgc	420
atcctcaccg cggaccggga cctttaccag cttcttttcgg agcgaatctc catccttcac	480
ccggagggtt acctgatcac cccggagtgg ctttgggaga agtatgggct taagccttcc	540
cagtgggtgg actaccgggc cttggccggg gacccttcgg acaacatccc cggcgtgaag	600
ggcatcgggg agaagacggc ggccaagctg atccgggagt ggggaagcct ggaaaacctt	660
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gaggacctca agctatccct ggagctatcc cgggtgcaca cggacttgct ccttcaggtg	780
gacttcgccc ggcgccggga gccggaccgg gaggggctta aggccttttt ggagaggctg	840
gagttcgga gctcctcca cgagttcggc ctgttgga gcccgggtggc ggcggaggaa	900
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atgtgggcgg agcttaacgc cttggccgcc gcctggggcg gccgcgtgca ccgggcagca	1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctctgccccg gggacgaccc catgctcctc	1140
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gagcttaggc ttccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
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gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag	1920
gacatccaca cccagaccgc aagctggatg ttcggcgctc ccccgagggc cgtggacccc	1980
ctgatgcgcc gggcggccaa gacggtgaac ttcggcgctc tctacggcat gtccgcccat	2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac	2100
ttccaaagct tcccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag	2160

cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgacct caacgcccgg 2220
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 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
 gcccgcatgc tcctccaggt cgccaacgag ctctccttgg agggccccca agcgcgggcc 2400
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
 caccac 2526

<210> 472

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 472

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	145	150	155	160

Pro Glu Gly Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro
 180 185 190
 Ser Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala
 195 200 205
 Lys Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu
 210 215 220
 Glu Gln Val Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met
 225 230 235 240
 Glu Asp Leu Lys Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu
 245 250 255
 Leu Leu Gln Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Lys Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 473

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 473

aagccactcc ggggtgatca ggtaacc

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<210> 474

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 474

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<210> 475

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 475

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ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc

120

caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg

180

gtgatcgtgg tctttgacgc cgaggccccc tccttcgcgc accagacctt cgaggcctac

240

aaggcggggc gggctccac ccccgaggac tttccccggc agcttgcct tatcaaggag

300

atggtggacc	ttttgggcct	ggagcgcctc	gaggtgccgg	gctttgaagc	ggatgacgtc	360
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cccaaggtgc	gggcctggat	agaaaagacc	ctggaggagg	ggaggaagcg	gggctacgtg	2160

gaaaccctct tcggaagaag gcgctacgtg cccgacctca acgcccgggt gaagagcgtc 2220
 agggaggccg cggagcgcat ggccttcaac atgcccgtcc agggcaccgc cgccgacctc 2280
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 gctttggcca aggaggccat ggagaaggcc tatccccctg ccgtgcccct ggaggtggag 2460
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<210> 476

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 476

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	1	5	10	15
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu	20	25	30	
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	35	40	45	
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	50	55	60	
Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	65	70	75	80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	85	90	95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val	100	105	110	
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	115	120	125	
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu	130	135	140	
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr	145	150	155	160
Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Glu	165	170	175	
Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp	Asn	Leu	180	185	190	

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu Leu Lys
 195 200 205
 Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val Lys
 210 215 220
 Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp Leu Arg
 225 230 235 240
 Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val
 245 250 255
 Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320
 Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg Ala Ala
 325 330 335
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
 405 410 415
 Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
 450 455 460
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525

Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
530 535 540
Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
545 550 555 560
His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
565 570 575
Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
580 585 590
Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala
595 600 605
Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
610 615 620
Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr
625 630 635 640
Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
645 650 655
Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly
660 665 670
Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
675 680 685
Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
690 695 700
Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val
705 710 715 720
Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
725 730 735
Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
740 745 750
Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
755 760 765
Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala
770 775 780
Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala
785 790 795 800
Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro
805 810 815
Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
820 825 830
His His His His His His
835

<210> 477
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 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 477
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 tggc 64
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 <211> 64
 <212> DNA
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 <220>
 <223> Synthetic
 <400> 478
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 ggtg 64
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 <212> DNA
 <213> Artificial Sequence
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 <400> 479
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 <210> 480
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 <220>
 <223> Synthetic

<400> 480
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 <212> DNA
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 gaaccgggtgc aggcgggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
 ggggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgc ccacgaggcc 240
 tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
 ctcatcaagg agctggtgga cctcctggggg ttaccgcgc tcgagggtccc cggctacgag 360
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ctcgccacgt tcgccggtt tccccgtaa gctctaaatc gggggctccc tttagggttc	3060
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<210> 482

<211> 1045

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 482

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	
			20					25					30			
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	
		35					40					45				
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	
	50					55					60					
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	
65					70					75					80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	
				85					90					95		
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	
			100					105					110			
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	
		115					120					125				
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	
	130					135					140					
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	
145					150				155						160	
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	
				165					170					175		
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	
			180					185					190			
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	
		195					200					205				
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	
	210					215					220					
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	
225					230					235					240	
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	
				245					250					255		

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His Val Asp Met Thr Met Ile
 835 840 845
 Thr Pro Ser Tyr Leu Gly Asp Thr Ile Glu Tyr Ser Ser Tyr Ala Ser
 850 855 860
 Ser Leu Val Pro Ser Ser Asp Pro Leu Val Thr Ala Ala Ser Val Leu
 865 870 875 880
 Glu Phe Cys Arg Tyr Pro Ser His Trp Arg Pro Leu Glu His Ala Ser
 885 890 895
 Arg Gly Pro Asn Ser Pro Tyr Ser Glu Ser Tyr Tyr Asn Ser Leu Ala
 900 905 910
 Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu
 915 920 925

Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu
 930 935 940
 Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly
 945 950 955 960
 Glu Trp Asp Ala Pro Cys Ser Gly Ala Leu Ser Ala Ala Gly Val Val
 965 970 975
 Val Thr Arg Ser Val Thr Ala Thr Leu Ala Ser Ala Leu Ala Pro Ala
 980 985 990
 Pro Phe Ala Phe Phe Pro Ser Phe Leu Ala Thr Phe Ala Gly Phe Pro
 995 1000 1005
 Arg Gln Ala Leu Asn Arg Gly Leu Pro Leu Gly Phe Arg Phe Arg
 1010 1015 1020
 Ala Leu Arg His Leu Asp Arg Lys Lys Leu Asp Leu Gly Asp Gly
 1025 1030 1035
 Ser Arg Ser Gly Pro Ser Pro
 1040 1045

<210> 483

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 483

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<210> 484

<211> 2517

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<213> Artificial Sequence

<220>

<223> Synthetic

<400> 484

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 gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggcccgggc cccacgccg gaggactttc cccggcaact cgcctcatc 300

aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatacctc	420
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gggtacctca tcccccggc ctggcctttg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccgggggt caagggcatc	600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg	720
aagctctcct gggacctggc caaggtgctc accgacctgc ccctggaggt ggacttcgcc	780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagagggt tgagtctggc	840
agcctcctcc acgagtccgg ccttctggaa agcccaagg ccctggagga ggccccctgg	900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc	960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg	1020
gcggggctaa aggacctcaa ggaggtcggg ggctcctcg ccaaggacct cgccgtcttg	1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc	1140
ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg	1200
gaggacgccc cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc	1260
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg	1320
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt	1380
tccctggagc ttgctggagg gatccgccgc ctcgaggagg aggtcttccg cttggcgggc	1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg	1500
cttcccgcct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg	1560
gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc	1620
aagctcaaga acacctacgt ggacccctc ccaagcctcg tccaccgag gacgggccgc	1680
ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc	1740
aacctgcaga acatccccgt ccgcaccccc ttgggccaga ggatccgccg ggccttcgtg	1800
gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc	1860
gcccacctct ccggggacga aaacctgac agggctctcc aggaggggaa ggacatccac	1920
accagaccg caagctggat gttcggcgtc cccccggagg ccgtggaccc cctgatgcgc	1980
cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc	2040
caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc	2100
ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac	2160

gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgcccg ggtgaagagc 2220
 gtcagggagg ccgcgaggcg catggccttc aacatgcccg tccagggcac cgccgcccac 2280
 ctcataaagc tcgcatggt gaagctcttc ccccgccctcc gggagatggg ggcccgcacg 2340
 ctctccagg tcgccaacga gctcctctg gaggcccccc aagcgcgggc cgaggaggtg 2400
 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460
 gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 485

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 485

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 486

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 486

gtggaccttc tgggctttac ccgcctcgag gccccg

36

<210> 487

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 487

cggggcctcg aggcgggtaa agcccagaag gtccac

36

<210> 488

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 488

Met Asn Ser Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu
20 25 30

Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe
35 40 45

Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
 100 105 110
 Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys
 115 120 125
 Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg
 130 135 140
 Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp
 145 150 155 160
 Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro
 165 170 175
 Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp
 180 185 190
 Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu
 195 200 205
 Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp
 225 230 235 240
 Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830

Ser Ala Lys Gly His His His His His His
 835 840

<210> 489

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 489

tttaccgcgcc tcgaggtgcc gggc

24

<210> 490

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 490

cggcacctcg aggcgggtaa agcccaaaag gtccac

36

<210> 491

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 491

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1 5 10 15
Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20 25 30
Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45
Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50 55 60
Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80
Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95
Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
100 105 110
Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115 120 125
Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
130 135 140
Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr
145 150 155 160
Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser
165 170 175
Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
180 185 190
Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg
195 200 205
Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys
210 215 220
Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys
225 230 235 240
Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
245 250 255
Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
260 265 270
Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
275 280 285
Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
290 295 300
Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
305 310 315 320

Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala
 325 330 335
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
 405 410 415
 Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
 450 455 460
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
 530 535 540
 Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590
 Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr
 625 630 635 640
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
 645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
 725 730 735
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 755 760 765
 Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala
 770 775 780
 Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala
 785 790 795 800
 Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro
 805 810 815
 Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
 820 825 830
 His His His His His His
 835

<210> 492

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 492

atcgtggtct ttgacgccga ggccccctcc ttcc

34

<210> 493

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 493
ggaaggagg ggcctcggcg tcaaagacca cgat

34

<210> 494

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 494

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	210	215	220	
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	225	230	235	240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

<400> 495
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtcct tgacgccgag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggccgggc cccacgccc gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggc caagggcatc 600
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<210> 496

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 496

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			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
			35				40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65				70					75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
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 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
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 340 345 350
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 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
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Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
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Gly His His His His His His
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<210> 497

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 497

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ccggtgcaga tgggtctacgg cttcgcccgg agcctcctca aggccttgaa ggaggacgga      180
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gcctacaagg cgggcccggc ccccaacccg gaggacttcc ccgccagct cgccttggtc      300
aagcggctgg tggaccttct gggcctggtc cgcctcgagg ccccggggta cgaggcggac      360
gacgtcctgg gcacctggc caagaaggcc gaaagggagg ggatggaggt gcgcacctc      420
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gagtggacgg aggacgcgcg ccaccgggcc ctctctcggg agaggctcca tcggaacctc     1260
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<210> 498

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 498

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			20					25					30		

Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe
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 Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val
 50 55 60
 Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
 65 70 75 80
 Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu
 100 105 110
 Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys
 115 120 125
 Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg
 130 135 140
 Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp
 145 150 155 160
 Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro
 165 170 175
 Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp
 180 185 190
 Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu
 195 200 205
 Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp
 225 230 235 240
 Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
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 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
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 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
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 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
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 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
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 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
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 Ser Ala Lys Gly His His His His His His
 835 840

<210> 499

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 499

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<210> 500

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 500

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20 25 30
Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45
Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50 55 60
Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80
Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95
Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
100 105 110
Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115 120 125
Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
130 135 140
Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr
145 150 155 160
Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser
165 170 175
Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
180 185 190
Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg
195 200 205
Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys
210 215 220
Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys
225 230 235 240
Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
245 250 255

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320
 Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala
 325 330 335
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
 405 410 415
 Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
 450 455 460
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
 530 535 540
 Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr
 625 630 635 640
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
 645 650 655
 Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
 725 730 735
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 755 760 765
 Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala
 770 775 780
 Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala
 785 790 795 800
 Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro
 805 810 815
 Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
 820 825 830
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 835

<210> 501

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 501
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ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg 240
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aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac 360
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accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
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aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggccacat ggacgatctg 720
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gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agaccccttg 1020
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cttccgcct tgaagaagac gaagaagaca ggcaagcgt ccaccagcg cgcggtgctg 1560
gaggccctac gggaggccca cccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620
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gcccacctct ccggggacga aaacctgatc agggctcttc aggaggggaa ggacatccac 1920
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 ctcctccagg tcgccaacga gctcctcctg gaggcccccc aagcgcgggc cgaggaggcg 2400
 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggcg 2460
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<210> 502

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 502

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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
			35				40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65				70					75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85				90						95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
	115						120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800

Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Gly His His His His His His
835

<210> 503

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 503

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34

<210> 504

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 504

ggaaggagg ggccctcggcg tcaaagacca cgat

34

<210> 505

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

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60

ggccaaccacc tggcctaccg caccttcacc gccctgaagg gcctcaccac cagccggggg

120

gagccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct caaggaggac

180

ggggacgcgg tgatcgtggt ctttgacgcc gagggcccct ctttcgccca cgaggcctac

240

gggggggtaca aggcggggccg ggccccccacg ccggaggact ttccccggca actcgccttc

300

atcaaggagc tgggtggacct cctgggggttc acgcgcctcg aggtcccggg ctacgaggcg	360
gacgacgtcc tggccagcct ggccaagaag gcggaaaagg agggctacga ggtccgcac	420
ctcaccgccg acaaagacct ttaccagctc ctttccgacc gcatccacgt cctccacccc	480
gaggggtacc tcatcacccc ggccctggctt tgggaaaagt acggcctgag gcccgaccag	540
tgggccgact accggggcct gaccggggac gagtccgaca accttcccgg ggtcaagggc	600
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gacctcatga agctcgccat ggtgaagctc ttcccccgcc tccgggagat gggggcccgcc 2340
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gtggcggtt tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag 2460
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<210> 506

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 506

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Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val
50 55 60
Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr
65 70 75 80
Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
85 90 95
Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg
100 105 110
Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala
115 120 125
Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
130 135 140
Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro
145 150 155 160
Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu
165 170 175
Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser
180 185 190

Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys
 195 200 205
 Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp
 210 215 220
 Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
 225 230 235 240
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
 305 310 315 320
 Ala Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
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 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830
 Lys Gly His His His His His His
 835 840

<210> 507
 <211> 36
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 507
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 <210> 508
 <211> 36
 <212> DNA
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 <223> Synthetic
 <400> 508
 aaagaggggc agcatcgcc cccaattcat ggtctg 36
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 ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
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 aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360
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 accgcgcaca aagaccttta ccagctcctt tccgaccgca tccagtcctt ccaccccgag 480
 gggtagctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600

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<210> 510

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 510

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85					90						95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165					170						175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
		180						185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
	195						200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
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 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
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 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
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 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
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 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
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 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
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 Gly His His His His His His
 835

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 <213> Artificial Sequence
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 <223> Synthetic
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 <210> 512
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 <400> 512
 gagggcccttc agggcaaaga aggtgcggtta ggc 33
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<210> 514

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 514

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
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 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 515

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 515

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33

<210> 516

<211> 33

<212> DNA

<213> Artificial Sequence

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33

<210> 517

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 517

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ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180

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gccgactacc gggccctgac cggggacgag tccgacaacc ttcccgggggt caagggcatc 600

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ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac	2160
gtggaaaccc tcttcggaag aaggcgctac gtgcccagacc tcaacgcccg ggtgaagagc	2220
gtcagggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac	2280
ctcatgaagc tcgccatggt gaagctcttc ccccgccctc gggagatggg ggcccgcctg	2340
ctcctccagg tcgccaacga gctcctcctg gagggccccc aagcgcgggc cgaggagggtg	2400
gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg	2460
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<210> 518

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 518

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
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Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305 310 315 320
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
325 330 335
Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
340 345 350
Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
355 360 365
Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400
Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
405 410 415
Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
420 425 430
Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
435 440 445
Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
450 455 460
Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
465 470 475 480
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495
Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
500 505 510
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525
Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
530 535 540
Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
545 550 555 560
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
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 820 825 830
 Gly His His His His His His
 835

<210> 519

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 519
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 <210> 520
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 520
 cgcctttcttg gccagggtgg ccaggacgtc gtc 33
 <210> 521
 <211> 2517
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 521
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 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgcagag gccccctcct tccgccacga ggccctacggg 240
 ggggtacaagg cgggcccgggc cccacgcgcg gaggactttc cccggcaact cgcctcatc 300
 aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac 360
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 accgccgaca aagaccttta ccagctcctt tccgaccgca tcacgtcct ccaccccgag 480
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 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggc caagggcatc 600
 ggggagaaga cggcgctcaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
 aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
 aaaaggcggg agcccgaacc ggagaggctt agggcctttc tggagaggct tgagtttggc 840
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960

gatcttcttg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agacccttg	1020
gcggggctaa	aggacctcaa	ggagggtccg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgctacctc	1140
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gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
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ctcatgaagc	tcgccatggt	gaagctcttc	ccccgcctcc	gggagatggg	ggcccgcgatg	2340
ctcctccagg	tcgccaacga	gtcctcctcg	gaggcccccc	aagcgcgggc	cgaggagggtg	2400
gcggcttttg	ccaaggaggc	catggagaag	gcctatcccc	tcgccgtgcc	cctggagggtg	2460
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<210> 522

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 522

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	
			20					25					30			
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	
		35					40					45				
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	
	50					55					60					
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	
65					70					75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	
				85					90					95		
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	
			100					105						110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	
		115					120					125				
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	
	130					135					140					
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	
145					150				155						160	
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	
				165				170						175		
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	
			180					185					190			
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu	
	195						200					205				
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	
	210					215					220					
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	
225					230				235						240	
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	
				245					250					255		
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	
			260					265					270			
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	
	275						280					285				

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 523

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 523

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33

<210> 524
 <211> 33
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 <210> 525
 <211> 2517
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 525
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 ccggtgcagg cgggtctacgg cttcgccaaag agcctcctca aggcctcaa ggaggacggg 180
 gacgcggtga tegtgtctt tgacgccgag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgcctcatc 300
 aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac 360
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 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
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gcccacctct ccggggacga aaacctgac agggctcttc aggaggggaa ggacatccac	1920
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cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc	2040
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ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac	2160
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gtcagggagg ccgcggagcg catggccttc aacatgcccc tccagggcac cgccgccgac	2280
ctcatgaagc tcgcatggt gaagctcttc cccgcctcc gggagatggg ggcccgcag	2340
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<210> 526

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 526

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	225	230	235	240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	245	250	255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala	260	265	270	
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	275	280	285	
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	290	295	300	
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	305	310	315	320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 527

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 527

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39

<210> 528

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 528
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 <211> 2517
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 ccgggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggcccggc cccacgccg gaggactttc cccggcaact cgccctcatc 300
 aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
 gggtagctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
 aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagagggt tgagtttggc 840
 agcctcctcc acgagttcgg ctttctggga ggggagaagc cccgggagga ggccccctgg 900
 cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020
 gcgggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080
 gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgctacctc 1140
 ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200
 gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
 ctcgaggggg aggagaagct cttttggctc taccacgagg tggaaaagcc cctctcccgg 1320
 gtcttgcccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380

tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440
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 cttcccgct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg 1560
 gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620
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 ttccccaagg tgccggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
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 gtcagggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tcgcatggt gaagctcttc cccgcctcc gggagatggg ggcccgcacg 2340
 ctctccagg tcgccaacga gctcctcctg gagggccccc aagcgcgggc cgaggaggtg 2400
 gcggctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460
 gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 530

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 530

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 531

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 531
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54

<210> 532

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 532
 gggccagggg gcctcctccc ggggcttctc ccctcccaga aggccgaact cgtg

54

<210> 533

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

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<400> 533

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ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgcccag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccggg cccacgcgc gaggactttc cccggcaact cgcctcatc 300
aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggagggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
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gatcttctgg ccctggccgc ctgcaggggc ggccgcgtgc accgggcagc agaccccttg 1020
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gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg 2460
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<210> 534

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 534

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75				80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105						110	

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780

Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
785 790 795 800

Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Gly His His His His His His
835

<210> 535

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 535
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33

<210> 536

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 536
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33

<210> 537

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120

ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg

180

gacgcggtga tcgtggtctt tgacgccgag gccccctcct tcggccacga ggcctacggg

240

gggtacaagg	cgggccgggc	ccccacgccg	gaggactttc	cccggcaact	cgccctcatc	300
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gacgtcctgg	ccagcctggc	caagaaggcg	gaaaaggagg	gctacgaggt	ccgcatcctc	420
accgccgaca	aagaccttta	ccagctcctt	tccgaccgca	tccacgtcct	ccaccccgag	480
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gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccggggg	caagggcatc	600
ggggagaaga	cggcgaggaa	gcttctgaag	gagtggggga	gcctggaagc	cctcctcaag	660
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gatcttctgg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agacccttg	1020
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 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggctg 2460
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<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 538

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			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165					170					175	

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
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 Gly His His His His His His
 835

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 <213> Artificial Sequence
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 <212> DNA
 <213> Artificial Sequence
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 <400> 540
 gctccccac tccttcagaa gcttctcgc cgtcttctcc cc 42
 <210> 541
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 gagccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct cagagaggac 180
 ggggacgcgg tgatcgtggt ctttgacgcc gagggcccct cttccgcca cgaggcctac 240
 ggggggtaca aggcgggccc ggccccacg ccggaggact ttccccggca actcgcctc 300
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cgccgggagg ccaagacggt gaacttcggc gtctctacg gcatgtccgc ccataggctc	2040
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<210> 542

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 542

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Ala Val
50 55 60

Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr
65 70 75 80

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
85 90 95

Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg
100 105 110

Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala
115 120 125

Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
130 135 140

Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro
145 150 155 160

Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu
165 170 175

Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser
180 185 190

Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys
195 200 205

Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp
210 215 220

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
 225 230 235 240
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
 305 310 315 320
 Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
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 Lys Gly His His His His His His
 835 840

<210> 543

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 543

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gagccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct cagagaggac	180
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accaagctca agaacaccta cgtggacccc ctccaagcc tcgtccaccc gaggacgggc	1680

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<210> 544

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 544

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
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Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Ala	Val
	50					55					60				
Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr
65					70					75				80	
Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg
			85						90					95	

Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg
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 Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala
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 Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
 130 135 140
 Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro
 145 150 155 160
 Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu
 165 170 175
 Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser
 180 185 190
 Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys
 195 200 205
 Leu Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp
 210 215 220
 Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
 225 230 235 240
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
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 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
 305 310 315 320
 Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
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 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
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 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
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 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
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 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
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 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
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 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
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 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780

Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
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Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
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Lys Gly His His His His His His
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<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<400> 545

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<211> 50

<212> DNA

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<223> Synthetic

<400> 546

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<210> 547

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 547

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33

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<400> 548
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18

<210> 549
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<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 550

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35 40 45
Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
50 55 60
Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
65 70 75 80
Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
85 90 95
Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
100 105 110
Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
115 120 125
Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
130 135 140
Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
145 150 155 160
Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
165 170 175
Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
180 185 190
Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
195 200 205
Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
210 215 220
Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Ala Asn Glu Gly Val
225 230 235 240
Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
245 250 255

Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
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<210> 551

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 551

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33

<210> 552

<211> 1008

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 552

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cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga	180
atcctataca gagtctccaa catgggtcgag gtgggaatca ggccggtgtt tgtattcgac	240
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gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct	360
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gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcgggaagc	540
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<210> 553

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 553

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			20					25					30		
Tyr	Gln	Phe	Ile	Ser	Ile	Ile	Arg	Gln	Pro	Asp	Gly	Thr	Pro	Leu	Lys
		35					40					45			
Asp	Ser	Gln	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg
	50					55					60				
Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp
65					70					75					80
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys
				85					90					95	
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly
			100					105					110		
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu
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	130					135						140			
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala
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Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
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 Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
 195 200 205
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
 210 215 220
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Arg Asn Glu Gly Val
 225 230 235 240
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
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 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335

<210> 554

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 554

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20

<210> 555

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 555

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 <213> Archaeoglobus fulgidus
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17

<210> 558

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<212> DNA

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<400> 558

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<400> 559

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<210> 560

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 560

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			20					25					30		
Tyr	Gln	Phe	Ile	Ser	Ile	Ile	Arg	Gln	Pro	Asp	Gly	Thr	Pro	Leu	Lys
		35					40					45			
Asp	Ser	Gln	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg
	50					55					60				
Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp
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Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys
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Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly
		100						105					110		
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu
		115					120					125			
Tyr	Ile	Val	Asp	Ser	Ala	Lys	Thr	Leu	Leu	Ser	Tyr	Met	Gly	Ile	Pro
	130					135					140				
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala
145					150					155				160	
Ala	Lys	Gly	Asp	Val	Glu	Tyr	Thr	Gly	Ser	Gln	Asp	Tyr	Asp	Ser	Leu
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 180 185 190
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
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 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
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 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
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 595 600 605
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 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 660 665 670
 Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp
 675 680 685
 Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 690 695 700
 Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 705 710 715 720
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile
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 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 740 745 750
 Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly
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 Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 785 790 795 800
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg
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 Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu
 820 825 830
 Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu
 835 840 845

Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
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Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His
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<210> 561

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 561
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21

<210> 562

<211> 36

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36

<210> 563

<211> 2619

<212> DNA

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60

120

180

240

300

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<210> 564

<211> 873

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 564

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 35 40 45
 Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
 50 55 60
 Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
 65 70 75 80
 Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
 85 90 95
 Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
 100 105 110
 Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
 115 120 125
 Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
 130 135 140
 Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
 145 150 155 160
 Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
 165 170 175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
 195 200 205
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
 210 215 220
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
 225 230 235 240
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
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 305 310 315 320
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 325 330 335
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 340 345 350
 Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His
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 Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg
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 Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu
 385 390 395 400
 Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp
 405 410 415
 Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu
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 Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His
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 Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu
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 His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu
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 Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr
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 Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg
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 625 630 635 640
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 Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp
 660 665 670
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 675 680 685
 Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val
 690 695 700
 Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro
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 Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro
 725 730 735
 Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg
 740 745 750
 Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu
 755 760 765
 Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe
 770 775 780
 Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met
 785 790 795 800
 Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu
 805 810 815
 Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu
 820 825 830
 Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu
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Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser
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Ala Lys Gly His His His His His His
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<210> 565

<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 565

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<210> 566

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 566

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Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp	65	70	75	80
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys	85	90	95	
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly	100	105	110	
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu	115	120	125	
Tyr	Ile	Val	Asp	Ser	Ala	Lys	Thr	Leu	Leu	Ser	Tyr	Met	Gly	Ile	Pro	130	135	140	
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala	145	150	155	160
Ala	Lys	Gly	Asp	Val	Glu	Tyr	Thr	Gly	Ser	Gln	Asp	Tyr	Asp	Ser	Leu	165	170	175	
Leu	Phe	Gly	Ser	Pro	Arg	Leu	Ala	Arg	Asn	Leu	Ala	Ile	Thr	Gly	Lys	180	185	190	
Arg	Lys	Leu	Pro	Gly	Lys	Asn	Val	Tyr	Val	Asp	Val	Lys	Pro	Glu	Ile	195	200	205	
Ile	Ile	Leu	Glu	Ser	Asn	Leu	Lys	Arg	Leu	Gly	Leu	Thr	Arg	Glu	Gln	210	215	220	
Leu	Ile	Asp	Ile	Ala	Ile	Leu	Val	Gly	Thr	Asp	Tyr	Asn	Glu	Gly	Val	225	230	235	240
Lys	Gly	Val	Gly	Val	Lys	Lys	Ala	Leu	Asn	Tyr	Ile	Lys	Thr	Tyr	Gly	245	250	255	
Asp	Ile	Phe	Arg	Ala	Leu	Lys	Ala	Leu	Lys	Val	Asn	Ile	Asp	His	Val	260	265	270	
Glu	Glu	Ile	Arg	Asn	Phe	Phe	Leu	Asn	Pro	Pro	Val	Thr	Asp	Asp	Tyr	275	280	285	
Arg	Ile	Glu	Phe	Arg	Glu	Pro	Asp	Phe	Glu	Lys	Ala	Ile	Glu	Phe	Leu	290	295	300	
Cys	Glu	Glu	His	Asp	Phe	Ser	Arg	Glu	Arg	Val	Glu	Lys	Ala	Leu	Glu	305	310	315	320

Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335
 Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe
 340 345 350
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala
 355 360 365
 Ala Cys Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala
 370 375 380
 Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser
 385 390 395 400
 Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro
 405 410 415
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
 420 425 430
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg
 435 440 445
 Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Leu Lys Arg Leu Glu
 450 455 460
 Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu
 465 470 475 480
 Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
 485 490 495
 Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg
 500 505 510
 Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 515 520 525
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro
 530 535 540
 Ala Ile Lys Lys Thr Gln Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 545 550 555 560
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 565 570 575
 Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu
 580 585 590
 Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 595 600 605
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 610 615 620
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 625 630 635 640
 Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln
 645 650 655

Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile
			660					665					670		
Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Glu	Thr	Ala	Ser	Trp
			675				680						685		
Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala
			690				695					700			
Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg
			705			710				715					720
Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Gln	Ala	Phe	Ile
				725					730						735
Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys
			740					745						750	
Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly
			755				760						765		
Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	Arg	Val	Lys	Ser	Val	Arg
			770			775						780			
Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala
			785			790				795					800
Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Glu
				805					810						815
Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	Ala	Asn	Glu	Leu	Val	Leu
			820					825					830		
Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala	Arg	Leu	Ala	Lys	Glu
			835				840						845		
Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val
			850			855					860				
Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu	His	His	His	His	His
			865		870					875					880

His

<210> 567

<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 567

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ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg	120
cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga	180
atcctataca gagtctccaa catggtcgag gtgggaatca ggccggtgtt tgtattcgac	240
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtctgag	300
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct	360
caggctgcag ggaggggttga cgagtacatt gttgactccg caaagacgct ttttaagttac	420
atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca	480
gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcgggaagc	540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttccccg caaaaatgtc	600
tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctgggtttg	660
acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgagggtgtg	720
aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg	780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttctg	840
aatctctctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc	900
atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttgag	960
aagctcaaag ctctgaagtc aaccagggcc acgcttgaga ggtgggttct ggaggaggcc	1020
ccctggcccc cgccggaagg ggccttcgtg ggcttcgtcc tctcccgccc cgagcccatg	1080
tgggcggagc ttaaagccct ggccgcctgc aggggcggcc gcgtccaccg ggcccccgag	1140
ccttataaag ccctcaggga cctgaaggag gcgcgggggc ttctcgccaa agacctgagc	1200
gttctggccc tgagggaagg ccttggcctc ccgcccggcg acgaccccat gctcctcgcc	1260
tacctcctgg acccttcgaa caccaccccc gagggggtgg cccggcgcta cggcggggag	1320
tggacggagg aggcggggga gcgggcccgc ctttccgaga ggctcttcgc caacctgtgg	1380
gggaggcttg agggggagga gaggtcctt tggttttacc gggagggtga gagggccctt	1440
tccgctgtcc tggcccatat ggaggccacg ggggtgcgcc tggacgtggc ctatctcagg	1500
gccttgtccc tggaggtggc cgaggagatc gccgcctcg aggcgaggt cttccgcctg	1560
gccggccacc ccttcaacct caactcccgg gaccagctgg aaagggtcct ctttgacgag	1620
ctagggttcc ccgccatcgg caagacggag aagaccggca agcgctccac cagcgccgcc	1680
gtcctggagg ccctccgca ggcccacccc atcgtggaga agatcctgca gtaccgggag	1740
ctaccaagc tgaagagcac ctacattgac cccttgccgg acctcatcca cccaggaagc	1800
ggccgcctcc acaccgctt caaccagacg gccacggcca cgggcaggct aagtagctcc	1860

gatcccaacc tccagaacat ccccgctccgc accccgcttg ggagaggat ccgcccgggcc 1920
 ttcacgcgcg aggggggtg gctattggtg gccctggact atagccagat agagctcagg 1980
 gtgctggccc acctctccgg cgacgagaac ctgatccggg tcttcaggga ggggcgggac 2040
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 ggggtacgtg agaccctctt cggccgcgcg cgctacgtgc cagacctaga ggcccgggtg 2340
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 gccgtggccc ggctggccaa ggaggtcatg gaggggggtg atcccctggc cgtgcccctg 2580
 gaggtggagg tggggatagg ggaggactgg ctctccgcca aggagcacca ccaccaccac 2640
 cac 2643

<210> 568

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 568

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 Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
 35 40 45
 Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
 50 55 60
 Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
 65 70 75 80
 Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
 85 90 95
 Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
 100 105 110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
 115 120 125
 Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
 130 135 140
 Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
 145 150 155 160
 Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
 165 170 175
 Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
 195 200 205
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
 210 215 220
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
 225 230 235 240
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320
 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335
 Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe
 340 345 350
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala
 355 360 365
 Ala Cys Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala
 370 375 380
 Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser
 385 390 395 400
 Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro
 405 410 415
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
 420 425 430
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg
 435 440 445

Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu
 450 455 460
 Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu
 465 470 475 480
 Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
 485 490 495
 Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg
 500 505 510
 Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 515 520 525
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro
 530 535 540
 Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 545 550 555 560
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 565 570 575
 Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu
 580 585 590
 Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 595 600 605
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 610 615 620
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 625 630 635 640
 Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln
 645 650 655
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 660 665 670
 Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp
 675 680 685
 Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 690 695 700
 Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 705 710 715 720
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile
 725 730 735
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 740 745 750
 Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly
 755 760 765
 Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg
 770 775 780

Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 785 790 795 800
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu
 805 810 815
 Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asn Glu Leu Val Leu
 820 825 830
 Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu
 835 840 845
 Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
 850 855 860
 Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu His His His His His
 865 870 875 880

His

<210> 569

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 569

gagcggataa caatttcaca cagg

24

<210> 570

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 570

tgccccggtgc acgcgggcgc ccctgcaggc

30

<210> 571

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 571
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gtgatcgtgg tgtttgacgc caaggcccc tccttccgcc accagacctt cgaggcctac 240
aaggcggggc gggctccac ccccgaggac tttccccggc agcttgccct tatcaaggag 300
atggtggacc ttttgggcct ggagcgctc gaggtgccgg gctttgaagc ggatgacgtc 360
ctggctaccc tggccaagaa ggccgaaaag gagggctacg aggtccgcat cctcaccgcc 420
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 ttcggaagaa ggcgctacgt gcccgcctc aacgcccggg tgaagagcgt caggagggcc 2160
 gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc 2220
 gccatggtga agctcttccc ccgcctccgg gagatggggg ccgcgatgct cctccaggtc 2280
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 aaggaggcca tggagaaggc ctatcccctc gccgtgcccc tggaggtgga ggtggggatg 2400
 ggggaggact ggctttccgc caagggtcac caccaccacc accac 2445

<210> 572

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 572

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 20 25 30
 Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
 35 40 45
 Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
 50 55 60
 Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
 65 70 75 80
 Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
 85 90 95
 Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
 100 105 110
 Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
 130 135 140

Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
 145 150 155 160
 Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
 165 170 175
 Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
 180 185 190
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
 195 200 205
 Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
 210 215 220
 Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
 225 230 235 240
 Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255
 Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
 260 265 270
 Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
 275 280 285
 Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
 290 295 300
 Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
 305 310 315 320
 Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
 325 330 335
 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
 340 345 350
 Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365
 Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
 370 375 380
 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr
 420 425 430
 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445
 Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480

Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
 530 535 540
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
 545 550 555 560
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
 565 570 575
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
 580 585 590
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
 595 600 605
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
 625 630 635 640
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
 645 650 655
 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
 660 665 670
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
 675 680 685
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
 690 695 700
 Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
 705 710 715 720
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
 725 730 735
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
 740 745 750
 Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
 755 760 765
 Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
 770 775 780
 Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
 785 790 795 800
 Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
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<210> 573

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 573

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gtcaagcggc tgggtggacct tctgggcctg gtccgcctcg agggcccggg gtacgaggcg      360
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<210> 574

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 574

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			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val
	50					55					60				
Ile	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr
65					70					75				80	

Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	
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Gln	Leu	Ala	Leu	Val	Lys	Arg	Leu	Val	Asp	Leu	Leu	Gly	Leu	Val	Arg	
			100					105					110			
Leu	Glu	Ala	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Gly	Thr	Leu	Ala	
		115					120					125				
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	
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Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	
145					150					155					160	
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	
			165						170					175		
Lys	Pro	Ser	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	
			180					185					190			
Asp	Asn	Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	
	195						200					205				
Leu	Ile	Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	
	210					215					220					
Arg	Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	
225					230					235					240	
Leu	Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	
			245						250					255		
Glu	Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	
		260						265					270			
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	
		275					280					285				
Leu	Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	
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Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	
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Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val	His	Arg	
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Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly	
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Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp	
		355					360					365				
Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	
	370					375					380					
Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	
385					390					395					400	
Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	
				405					410					415		

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780

Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815

Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
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Lys Gly His His His His His His
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<210> 575

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 575

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<210> 576

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 576

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	1	5	10	15
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Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	35	40	45	
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	50	55	60	
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	65	70	75	80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	85	90	95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	Glu	Val	100	105	110	
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	115	120	125	
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	Asp	Leu	130	135	140	
Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	Gly	Tyr	145	150	155	160
Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Asp	165	170	175	
Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	Asn	Leu	180	185	190	
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	Glu	195	200	205	
Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	Lys	210	215	220	
Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys	Leu	225	230	235	240
Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp	245	250	255	
Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Glu	Lys	Pro	Arg	Glu	260	265	270	
Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Leu	Leu	275	280	285	
Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	290	295	300	
Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	305	310	315	320

Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
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 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
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 Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365
 Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
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 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr
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 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
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 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
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 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
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 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
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 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
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 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
 595 600 605
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
 625 630 635 640
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
 645 650 655

Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
 660 665 670
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
 675 680 685
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
 690 695 700
 Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
 705 710 715 720
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
 725 730 735
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
 740 745 750
 Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
 755 760 765
 Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
 770 775 780
 Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
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 805 810 815

<210> 577

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 577

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<210> 578

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 578

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	50	55	60	
Ile	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	65	70	75	80
Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	85	90	95	
Gln	Leu	Ala	Leu	Val	Lys	Arg	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	100	105	110	
Leu	Glu	Ala	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Gly	Thr	Leu	Ala	115	120	125	
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	130	135	140	
Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	145	150	155	160
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	165	170	175	
Lys	Pro	Ser	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	180	185	190	
Asp	Asn	Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	195	200	205	
Leu	Ile	Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	210	215	220	

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
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 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
 305 310 315 320
 Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
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 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830
 Lys Gly His His His His His His
 835 840

<210> 579

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 579

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caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
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atggtggacc ttttgggcct ggagcgcctc gagtgccgg gctttgaagc ggatgacgtc	360
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gacaaagacc ttaccagct cttttccgac cgcattccacg tctccacccc cgaggggtac	480
ctcatcacc cggcctggct ttgggaaaag tacggcctga ggcccgacca gtgggcccgc	540
taccgggccc tgaccgggga cgagtccgac aaccttcccg gggtaaggg catcggggag	600
aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg	660
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cgggagcccg accgggaggg ggagaagccc cgggaggagg cccctggcc cccgcccga	840
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acctacgtgg accccctccc aagcctcgtc caccgagga cgggcgcct ccacaccgc	1620
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<210> 580

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 580

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
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Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr
65					70					75				80	
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
			85						90					95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val
			100					105						110	

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
 130 135 140
 Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
 145 150 155 160
 Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
 165 170 175
 Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
 180 185 190
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
 195 200 205
 Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
 210 215 220
 Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
 225 230 235 240
 Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255
 Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
 260 265 270
 Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
 275 280 285
 Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
 290 295 300
 Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
 305 310 315 320
 Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
 325 330 335
 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
 340 345 350
 Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365
 Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
 370 375 380
 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr
 420 425 430
 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445

Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480
 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
 530 535 540
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
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 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
 565 570 575
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
 580 585 590
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
 595 600 605
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
 625 630 635 640
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
 645 650 655
 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
 660 665 670
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
 675 680 685
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
 690 695 700
 Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
 705 710 715 720
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
 725 730 735
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
 740 745 750
 Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
 755 760 765

Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
770 775 780

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
785 790 795 800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
805 810 815

<210> 581

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 581

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caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg      180
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gggctagacc tcgtgcccgg ggacgacccc atgctcctcg cctacctcct ggacccttcg      1080
aacaccaccc ccgagggggg ggcgcggcgc tacggggggg agtggacgga ggacgccgcc      1140
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<210> 582

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 582

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Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
 35 40 45
 Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
 50 55 60
 Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
 65 70 75 80
 Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
 85 90 95
 Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
 100 105 110
 Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
 130 135 140
 Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
 145 150 155 160
 Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
 165 170 175
 Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
 180 185 190
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
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 Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
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 Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
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 Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255
 Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
 260 265 270
 Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
 275 280 285
 Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
 290 295 300
 Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
 305 310 315 320
 Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
 325 330 335
 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
 340 345 350
 Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365

Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
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 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr
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 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445
 Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480
 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
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 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
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 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
 545 550 555 560
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
 565 570 575
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
 580 585 590
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
 595 600 605
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
 625 630 635 640
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
 645 650 655
 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
 660 665 670
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
 675 680 685
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
 690 695 700

Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala
705					710					715					720
Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp
				725					730					735	
Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met
			740					745					750		
Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala
		755					760					765			
Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met
	770					775					780				
Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met
785					790					795					800
Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Gly	His	His	His	His	His	His	His
				805					810					815	

<210> 583

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 583

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gagccggtcc aggcggtgta cggggttgcc aagagccttt tgaaggcgct aagagaagac	180
ggggacgcgg tgatcgtggt ctttgacgcc gagggccct ccttcgccca cgaggcctac	240
ggggggtaca aggcggggcg ggctcccacc cccgaggact ttccccggca gcttgccctt	300
atcaaggagc tgggtggacct cctggggttt accgcctcg aggtccccgg ctacgaggcg	360
gacgacgttc tcgccacct ggccaagaag gcggaaaagg aggggtacga ggtgcgcac	420
ctcaccgccg acaaagacct ttaccagctc ctttcgcacc gcatccacgt cctccacccc	480
gaggggtacc tcatcacccc ggcttggtt tgggaaaagt acggcctgag gcccgaccag	540
tgggcccact accgggccct gaccggggac gagtccgaca accttcccgg ggtcaagggc	600
atcggggaga agaccgcct caagctctc aaggagtggg ggagcctgga agccctctc	660
aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggcca catggacgat	720
ctgaagctct cctgggacct ggccaaggtg cgcaccgacc tgcccctgga ggtggacttc	780
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gccgatcttc tggccctggc cgcctgcagg ggcggccgcg tgcaccgggc agcagacccc	1020
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ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgccctac	1140
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cgcctcgagg gggaggagaa gctcctttgg ctctaccacg aggtggaaaa gcccctctcc	1320
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gtggcggctt tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag	2460
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<210> 584

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 584

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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Ala	Val
	50					55					60				
Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr
65					70					75					80
Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg
				85					90					95	
Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg
			100					105					110		
Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala
		115					120					125			
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp
	130					135					140				
Lys	Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro
145					150					155					160
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu
			165						170					175	
Arg	Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser
			180					185					190		
Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys
		195					200					205			
Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp
	210					215						220			
Arg	Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp
225					230					235					240
Leu	Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu
				245					250					255	

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
 305 310 315 320
 Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590

Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	
	595						600					605				
Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	
	610					615					620					
Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	
625					630					635					640	
His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	
				645					650					655		
Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	
			660					665					670			
Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	
	675						680					685				
Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	
	690					695					700					
Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	
705					710					715					720	
Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	
				725					730					735		
Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	
			740					745					750			
Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	
	755						760					765				
Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	
	770					775					780					
Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	
785					790				795						800	
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	
				805					810					815		
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	
			820					825					830			
Lys	Gly	His	His	His	His	His	His									
	835						840									

<210> 585

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 585
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<210> 586

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 586

Met	Glu	Phe	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	1	5	10	15
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	Gly	Leu	20	25	30	
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	35	40	45	
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	50	55	60	
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Gly	Tyr	65	70	75	80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	85	90	95	
Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	Glu	Val	100	105	110	
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	115	120	125	
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Gly	Asp	Arg	Asp	Leu	130	135	140	

Tyr Gln Leu Val Ser Asp Arg Val Ala Arg Pro Glu Gln Trp Val Asp
145 150 155 160
Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile Pro Gly Val Lys
165 170 175
Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp Gly Ser
180 185 190
Val Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala Ile Arg
195 200 205
Glu Lys Ile Leu Ala His Met Glu Asp Leu Lys Leu Ser Leu Glu Leu
210 215 220
Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val Asp Leu Ala Gln Gly
225 230 235 240
Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe Leu Glu Arg Leu Glu
245 250 255
Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Val Ala
260 265 270
Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Tyr
275 280 285
Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Asn Ala Leu Ala
290 295 300
Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly
305 310 315 320
Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala
325 330 335
Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro
340 345 350
Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
355 360 365
Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg
370 375 380
Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu
385 390 395 400
Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu
405 410 415
Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val
420 425 430
Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg
435 440 445
Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
450 455 460
Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro
465 470 475 480

Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 485 490 495
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 500 505 510
 Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu
 515 520 525
 Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 530 535 540
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 545 550 555 560
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 565 570 575
 Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln
 580 585 590
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 595 600 605
 Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp
 610 615 620
 Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 625 630 635 640
 Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 645 650 655
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile
 660 665 670
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 675 680 685
 Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly
 690 695 700
 Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg
 705 710 715 720
 Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 725 730 735
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg
 740 745 750
 Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu
 755 760 765
 Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu
 770 775 780
 Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
 785 790 795 800
 Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
 805 810

<210> 587

<211> 2433

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 587

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caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagagaaga cggggatgtg      180
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gaccgcgacc tttaaccaact cgtctccgac cgcgtcgcca ggccggagca gtgggtggac      480
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aagacggcga ggaagcttct ggaggagtgg gggagcgtgg aagccctcct caagaacctg      600
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<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 588

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			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
			35				40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
			50			55					60				
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Gly	Tyr
65					70					75				80	

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 Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val
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 Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Gly Asp Arg Asp Leu
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 Tyr Gln Leu Val Ser Asp Arg Val Ala Arg Pro Glu Gln Trp Val Asp
 145 150 155 160
 Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile Pro Gly Val Lys
 165 170 175
 Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp Gly Ser
 180 185 190
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 195 200 205
 Glu Lys Ile Leu Ala His Met Glu Asp Leu Lys Leu Ser Leu Glu Leu
 210 215 220
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 225 230 235 240
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 Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Val Ala
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 Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp
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 725 730 735
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg
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<211> 2493

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<213> Artificial Sequence

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<400> 589

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<212> PRT

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<220>

<223> Synthetic

<400> 590

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Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Met	Val	Tyr	Gly	Phe	Ala	Arg	35	40	45	
Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	Val	Val	50	55	60	
Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	65	70	75	80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	85	90	95	
Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	Glu	Val	100	105	110	
Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	115	120	125	
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu	130	135	140	
Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	Gly	Tyr	145	150	155	160
Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Asp	165	170	175	
Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	Asn	Leu	180	185	190	
Ser	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	Glu	195	200	205	
Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	Lys	210	215	220	
Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys	Leu	225	230	235	240
Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp	245	250	255	
Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	Phe	Leu	260	265	270	
Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Pro	Leu	Glu	275	280	285	
Ser	Pro	Arg	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	290	295	300	
Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu	305	310	315	320

Asn Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Ala Asp
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 Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro
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 370 375 380
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 385 390 395 400
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 420 425 430
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 Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
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 595 600 605
 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
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 Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu
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Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met
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 Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
 740 745 750
 Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe
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<210> 616
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 gccctaaaca gatggaggcg 20
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26

<210> 768

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28

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caacgcttcc tccg

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ccgtcacgcc tccatctgtt tagg

24

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22

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<400> 778
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26

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28

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<223> Synthetic

<400> 784

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21

<210> 785

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<212> DNA

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<400> 785

ggccctaaac agatgagtga tc

22

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14

<210> 788

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14

<210> 793

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<222> (4)..(4)

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14

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<400> 800

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<210> 801
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<223> Synthetic

<400> 801
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23

<210> 802

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<400> 802
ccaacctgct gagaggcg

18

<210> 803

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<400> 803
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28

<210> 804

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 <210> 807
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 <210> 809
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<210> 812
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 <400> 815
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<210> 816
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 <400> 817
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 ccagtgatga ttttcaccag gcaagta 27
 <210> 819
 <211> 23
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 <400> 819
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 <210> 820
 <211> 17
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 ttcaatgagg aggaggc 17
 <210> 821
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 <400> 821
 cggaagaagc agttggaggc gtgacggt 28
 <210> 822
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 <222> (4)..(4)
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 <223> Synthetic
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 ccgtcacgcc tcctcctcat tgaata 26
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 ccgtcacgcc tcctcctcat tgaatt 26
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<210> 827
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 <213> Artificial Sequence
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 <400> 828
 gattcaatga ggaggaggc 19
 <210> 829
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<221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
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 <211> 26
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 <400> 831
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 ccgtcacgcc tccttcggag tttggtt 27
 <210> 833
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 <400> 833
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 <223> Synthetic
 <400> 834
 aacccaaact ccgaaggcgg cgtg 24
 <210> 835
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 <400> 835
 cggaagaagc agttggaggc gtgacggt 28
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 <223> Synthetic
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 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
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 <210> 837
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 <400> 837
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<210> 838
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 tggagtgagt gttcaagtct tcggaga 27
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 <223> Synthetic
 <400> 840
 gacaagcaaa cccaaagagg cg 22
 <210> 841
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 cggaagaagc agttggaggc gtgacggc 28

<210> 842
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 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
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 <223> Synthetic
 <400> 843
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 <210> 844
 <211> 26
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 844
 cctgtctcgc tgccttcgga gtttgg 26
 <210> 845
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 <212> DNA

<213> Artificial Sequence
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 <223> Synthetic
 <400> 845
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 <210> 846
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 cccaaactcc gaaggcagcg 20
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 cggaggaagc agttggcagc gagacagg 28
 <210> 848
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 <223> Synthetic
 <220>
 <221> modified_base
 <222> (26)..(26)
 <223> The modified nucleotide at this position is amino-deoxy adenosine
 <400> 848
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<210> 849

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<220>

<221> modified_base

<222> (22)..(22)

<223> The modified nucleotide at this position is amino-deoxy adenosine

<400> 849

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28

<210> 850

<211> 28

<212> DNA

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<220>

<223> Synthetic

<220>

<221> modified_base

<222> (18)..(18)

<223> The modified nucleotide at this position is amino-deoxy adenosine

<400> 850

cggaggaagc agttggcagc gagacagg

28

<210> 851

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (22)..(22)

<223> The modified nucleotide at this position is amino-deoxy adenosine

<220>

<221> modified_base

<222> (26)..(26)

<223> The modified nucleotide at this position is amino-deoxy adenosine

<400> 851

cggaggaagc agttggcagc gagacagg

28

<210> 852

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<220>

<221> modified_base

<222> (18)..(18)

<223> The modified nucleotide at this position is amino-deoxy adenosine

<220>

<221> modified_base

<222> (26)..(26)

<223> The modified nucleotide at this position is amino-deoxy adenosine

<400> 852

cggaggaagc agttggcagc gagacagg

28

<210> 853

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<212> DNA

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 <222> (18)..(18)
 <223> The modified nucleotide at this position is amino-deoxy adenosine
 <220>
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 <222> (22)..(22)
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 <400> 853
 cggaggaagc agttggcagc gagacagg 28
 <210> 854
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 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 854
 caacgcttcc tccg 14
 <210> 855
 <211> 28
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<400> 855
 gccgtcacgc ctctgggaca cttgctgc 28
 <210> 856
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<400> 896

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 ccagcagtaa atgctccagt tgtaga 26
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19

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27

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13

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<223> Synthetic

<400> 917

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26

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 <400> 919
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23

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27

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24

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26

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<400> 1017

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26

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30

<210> 1021

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29

<210> 1053

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<400> 1053

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32

<210> 1054

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29

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 cgagggttttc caaggagttg ttta 24
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 <400> 1065
 ccctggatca gatttagaga gc 22

<210> 1066
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 atcttagcta acgggaggcg 20
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 <400> 1075
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	agatccctgg atcagattta gagagctc	28
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 agaggtagaa acgaggtttt ccaaggaga 29
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 ctaagatccc tggatcagat ttagagag 28
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